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Genome Sequence of *Bradyrhizobium japonicum* E109, One of the Most Agronomically Used Nitrogen-Fixing Rhizobacteria in Argentina

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We present here the complete genome sequence of *Bradyrhizobium japonicum* strain E109, one of the most used rhizobacteria for soybean inoculation in Argentina since the 1970s. The genome consists of a 9.22-Mbp single chromosome and contains several genes related to nitrogen fixation, phytohormone biosynthesis, and a rhizospheric lifestyle.

Received 29 December 2014 **Accepted** 5 January 2015 **Published** 19 February 2015

Citation Torres D, Revale S, Obando M, Maroniche G, Paris G, Perticari A, Vazquez M, Wisniewski-Dyé F, Martínez-Abarca F, Cassán F. 2015. Genome sequence of *Bradyrhizobium japonicum* E109, one of the most agronomically used nitrogen-fixing rhizobacteria in Argentina. Genome Announc 3(1):e01566-14. doi:10.1128/genomeA.01566-14.

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The soybean-*Bradyrhizobium* symbiosis is considered one of the most efficient in fixing N_2 and probably the greatest in economic importance around the world (1). The agronomic cultivation of soybeans (*Glycine max* L.) affects >20 million ha in Argentina, where at least 85%, on average, are biologically treated with bradyrhizobia (2). In the 1970s, several strains belonging to the genus *Bradyrhizobium* were received in Argentina from different collections around the world to be evaluated under agronomical conditions, including strain 2860 (previously named USDA138 and corresponding to the *Bradyrhizobium japonicum* USDA6 serogroup), sent by C. N. Hale from the Department of Scientific and Industrial Research (DSIR) in New Zealand. After evaluation, selection, and reisolation from soybean nodules, the strain was renamed E109. To date, *B. japonicum* E109 has been the only strain recommended by the Instituto Nacional de Tecnología Agropecuaria (INTA) for soybean inoculation due to its capacity to effectively colonize the plant and fix nitrogen, increasing crop productivity (3). Together with this ability, alternative mechanisms have been proposed to explain the growth promotion, especially in nonlegumes, such as phosphate solubilization (4), siderophore production (5), systemic resistance induction (6), and phytohormone biosynthesis (7–9).

We announce here the complete annotated genome sequence of *B. japonicum* E109. The sequence was obtained using a combined whole-genome shotgun and 8-kb paired-end strategy with a 454 GS FLX Titanium pyrosequencer at the Instituto de Agrobiotecnología Rosario (INDEAR) (Argentina), resulting in a 24-fold genome coverage. The sequencing reads were *de novo* assembled (Newbler version 2.9), resulting in 142 contigs ordered in 4 scaffolds (>737 kbp each; N_{50}, 4,081,299 bp). Intra- and interscaffold gap closures were achieved by a detailed observation of the relevant sequencing reads using the Geneious R7 software platform (10). The absence of plasmids is a common feature of *Bradyrhizobium* genomes (11–13), and in agreement with the bioinformatics data, pulsed-field gel electrophoresis (PFGE) analysis of total DNA revealed the presence of a unique chromosome. The genome size is 9,224,208 bp, and the G+C content, in agreement with this bacterial species, is 63.6%.

Genome annotation was done using the NCBI Prokaryotic Genomes Annotation Pipeline (PGAP) (14). The complete genome consists of 8.233 protein-coding sequences. Similarly to other species of the *Bradyrhizobium* genus, *B. japonicum* E109 contains two identical and complete ribosomal operons. A total of 54 tRNA genes representing 45 tRNA species were identified. In agreement with the genome sequence of USDA6, the presence of a 645-kb DNA region with low G+C content (59.0%) was revealed to be reminiscent of a symbiotic island, which includes most of the *nod*, *nif*, and *fixes* genes. The putative genes involved in other plant growth-promoting mechanisms, such as phytohormone production, were determined using the RAST annotation server (15) and KAAS (16).

The *B. japonicum* E109 genome contains genes related to type II and VI secretion systems, nitrogen fixation, phytohormone biosynthesis, and a rhizospheric lifestyle. The genome sequence of E109 provides a genomic basis for in-depth comparative genome analyses to elucidate the specific mechanisms of *Bradyrhizobium*-plant interactions.

Nucleotide sequence accession number. The complete genome sequence of *B. japonicum* E109 is available at NCBI GenBank under the accession no. CP010313.

ACKNOWLEDGMENTS

This work was supported by the Consejo Nacional de Investigación Científico-Tecnológica (CONICET), Argentina, the Fondo Nacional para la Investigación Científico Tecnológica (FONCyT), the Ministerio de Ciencia y Tecnología de la República Argentina (MINCyT), and the Spanish Ministerio de Ciencia e Innovación in the Programme Consolider-Ingenio (CSD2009-0006), including the European Regional Develop-

ment Funds (ERDF) and the Biotechnology and Biosciences Research Council (BBSRC). D.T. and F.C. are recipients of a doctoral fellowship grant from CONICET.

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